49   7/11/06

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rag.
start

```
                          GenCore version 5.1.9
                 Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:           July 11, 2006, 06:34:19 ; Search time 22 Seconds
                                           (without alignments)
                                           7519.132 Million cell updates/sec

Title:            US-10-785-114-6
Perfect score:    2202
Sequence:         1 atgaacaacttgctgtgctg..........taaaaataagctgcttataa 1206

Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0

Searched:         2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      5179358

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10785114/runat_11072006_062819_21385/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10785114_@CGN_1_1_165_@runat_11072006_062819_21385 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :        A_Geneseq_8:*
                  1:  geneseqp1980s:*
                  2:  geneseqp1990s:*
                  3:  geneseqp2000s:*
                  4:  geneseqp2001s:*
                  5:  geneseqp2002s:*
                  6:  geneseqp2003as:*
                  7:  geneseqp2003bs:*
                  8:  geneseqp2004s:*
                  9:  geneseqp2005s:*
                  10:  geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2201	99.9	401	2	AAR99925	Aar99925 Full leng
2	2201	99.9	401	2	AAW53239	Aaw53239 Human OCI
3	2201	99.9	401	3	AAY88622	Aay88622 Osteoclas
4	2201	99.9	401	6	ABP70997	Abp70997 Human ost
5	2201	99.9	401	7	ADD37427	Add37427 Human ost
6	2201	99.9	401	8	ADQ68056	Adq68056 Human ost
7	2201	99.9	401	8	ADT07096	Adt07096 Human ost
8	2195	99.7	401	2	AAY05742	Aay05742 Tumour ne
9	2195	99.7	401	2	AAW95030	Aaw95030 Tumour ne
10	2195	99.7	401	2	AAW83926	Aaw83926 Human FTH
11	2195	99.7	401	3	AAB18715	Aab18715 A human t
12	2195	99.7	401	4	AAB60570	Aab60570 Human TNF
13	2195	99.7	401	6	AAE36245	Aae36245 Human TRA
14	2195	99.7	401	6	AAO31135	Aao31135 Human TRA
15	2195	99.7	401	7	ADD01625	Add01625 Human ost
16	2195	99.7	401	7	ADF16158	Adf16158 Human alb
17	2195	99.7	401	7	ADF16153	Adf16153 Human alb
18	2195	99.7	401	7	ADF16151	Adf16151 Human alb
19	2195	99.7	401	7	ADF15231	Adf15231 Human alb
20	2195	99.7	401	7	ADF16152	Adf16152 Human alb
21	2195	99.7	401	7	ADF16154	Adf16154 Human alb
22	2195	99.7	401	7	ADF16155	Adf16155 Human alb
23	2195	99.7	401	7	ADF16156	Adf16156 Human alb
24	2195	99.7	401	7	ADF15230	Adf15230 Human alb
25	2195	99.7	401	7	ADF15244	Adf15244 Human alb
26	2195	99.7	401	7	ADF16157	Adf16157 Human alb
27	2195	99.7	401	8	ADK82154	Adk82154 Human TRA
28	2195	99.7	401	9	ADY34172	Ady34172 Human TRA
29	2195	99.7	401	9	AEA27537	Aea27537 Human TR1
30	2195	99.7	401	9	AEA55153	Aea55153 Human TRA
31	2195	99.7	401	9	AEB19868	Aeb19868 Human ost
32	2195	99.7	401	9	AED07227	Aed07227 Human tum
33	2195	99.7	401	9	AED07297	Aed07297 Human tum
34	2195	99.7	401	9	AED07408	Aed07408 Human tum
35	2195	99.7	986	7	ADF15016	Adf15016 Human alb
36	2195	99.7	986	7	ADF15030	Adf15030 Human alb
37	2191	99.5	401	2	AAR99931	Aar99931 Mutated O
38	2191	99.5	401	2	AAR99932	Aar99932 Mutated O
39	2188	99.4	399	2	AAR99942	Aar99942 Mutated O
40	2187	99.3	401	2	AAW38345	Aaw38345 Human ost
41	2187	99.3	401	3	AAY43400	Aay43400 Osteoprot
42	2187	99.3	401	4	AAB66976	Aab66976 Human OPG
43	2187	99.3	401	5	ABG71823	Abg71823 Wild type
44	2187	99.3	401	6	ABP55109	Abp55109 Human ost
45	2187	99.3	401	6	AAE34363	Aae34363 Human ost

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rai.

<u>start</u>

<u>Go Back to previous page</u>

```
                        GenCore version 5.1.9
                 Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:            July 11, 2006, 06:40:14 ; Search time 5.2 Seconds
                                              (without alignments)
                                           6090.112 Million cell updates/sec


Title:             US-10-785-114-6
Perfect score:     2202
Sequence:          1 atgaacaacttgctgtgctg..........taaaaataagctgcttataa 1206

Scoring table:     BLOSUM62
                   Xgapop 10.0 , Xgapext  0.5
                   Ygapop 10.0 , Ygapext  0.5
                   Fgapop  6.0 , Fgapext  7.0
                   Delop   6.0 , Delext   7.0

Searched: ·        650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:       1301182

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10785114/runat_11072006_062826_21503/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss02h -USER=US10785114_@CGN_1_1_37_@runat_11072006_062826_21503
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :         Issued_Patents_AA:*
                   1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                   2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                   3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                   4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                   5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                   6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                   7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2201	99.9	401	2	US-10-232-858-5	Sequence 5, Appli
2	2201	99.9	401	2	US-09-338-063A-5	Sequence 5, Appli
3	2195	99.7	401	2	US-09-153-927-1	Sequence 1, Appli
4	2195	99.7	401	2	US-09-072-993C-1	Sequence 1, Appli
5	2191	99.5	401	2	US-10-232-858-62	Sequence 62, Appl
6	2191	99.5	401	2	US-10-232-858-63	Sequence 63, Appl
7	2191	99.5	401	2	US-10-232-858-64	Sequence 64, Appl
8	2191	99.5	401	2	US-10-232-858-65	Sequence 65, Appl
9	2191	99.5	401	2	US-10-232-858-66	Sequence 66, Appl
10	2191	99.5	401	2	US-09-338-063A-62	Sequence 62, Appl
11	2191	99.5	401	2	US-09-338-063A-63	Sequence 63, Appl
12	2191	99.5	401	2	US-09-338-063A-64	Sequence 64, Appl
13	2191	99.5	401	2	US-09-338-063A-65	Sequence 65, Appl
14	2191	99.5	401	2	US-09-338-063A-66	Sequence 66, Appl
15	2188	99.4	399	2	US-10-232-858-73	Sequence 73, Appl
16	2188	99.4	399	2	US-09-338-063A-73	Sequence 73, Appl
17	2187	99.3	401	2	US-08-974-022-6	Sequence 6, Appli
18	2187	99.3	401	2	US-09-042-785A-12	Sequence 12, Appl
19	2187	99.3	401	2	US-08-795-445A-6	Sequence 6, Appli
20	2187	99.3	401	2	US-08-795-447A-6	Sequence 6, Appli
21	2187	99.3	401	2	US-08-974-186-6	Sequence 6, Appli
22	2187	99.3	401	2	US-08-795-446B-6	Sequence 6, Appli
23	2187	99.3	401	2	US-08-706-945D-128	Sequence 128, App
24	2187	99.3	401	2	US-08-577-788C-6	Sequence 6, Appli
25	2187	99.3	401	2	US-08-577-788C-56	Sequence 56, Appl
26	2187	99.3	401	2	US-09-064-832-2	Sequence 2, Appli
27	2183	99.1	401	3	US-09-613-591F-125	Sequence 125, App
28	2155	97.9	393	2	US-10-232-858-79	Sequence 79, Appl
29	2155	97.9	393	2	US-09-338-063A-79	Sequence 79, Appl
30	2152.5	97.8	394	2	US-10-232-858-9	Sequence 9, Appli
31	2152.5	97.8	394	2	US-09-338-063A-9	Sequence 9, Appli
32	2146	97.5	391	2	US-10-232-858-106	Sequence 106, App
33	2146	97.5	391	2	US-09-338-063A-106	Sequence 106, App
34	2087	94.8	380	2	US-10-232-858-4	Sequence 4, Appli
35	2087	94.8	380	2	US-09-338-063A-4	Sequence 4, Appli
36	2070	94.0	380	3	US-09-613-591F-139	Sequence 139, App
37	1976	89.7	364	2	US-08-706-945D-142	Sequence 142, App
38	1972.5	89.6	362	2	US-10-232-858-11	Sequence 11, Appl
39	1972.5	89.6	362	2	US-09-338-063A-11	Sequence 11, Appl
40	1956	88.8	363	2	US-10-232-858-69	Sequence 69, Appl
41	1956	88.8	363	2	US-09-338-063A-69	Sequence 69, Appl
42	1944	88.3	351	2	US-10-232-858-74	Sequence 74, Appl
43	1944	88.3	351	2	US-09-338-063A-74	Sequence 74, Appl
44	1933	87.8	359	2	US-10-232-858-70	Sequence 70, Appl
45	1933	87.8	359	2	US-09-338-063A-70	Sequence 70, Appl

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rapbm.

start

```
                         GenCore version 5.1.9
              Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:            July 11, 2006, 06:41:44 ; Search time 24.7 Seconds
                                             (without alignments)
                                           6785.066 Million cell updates/sec

Title:             US-10-785-114-6
Perfect score:     2202
Sequence:          1 atgaacaacttgctgtgctg..........taaaaataagctgcttataa 1206

Scoring table:     BLOSUM62
                   Xgapop 10.0 , Xgapext  0.5
                   Ygapop 10.0 , Ygapext  0.5
                   Fgapop  6.0 , Fgapext  7.0
                   Delop   6.0 , Delext   7.0

Searched:          2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:       4195594

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=x1h
-Q=/abss/ABSSWEB_spool/US10785114/runat_11072006_062829_21549/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=rapbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10785114_@CGN_1_1_156_@runat_11072006_062829_21549 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :         Published_Applications_AA_Main:*
                   1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                   2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                   3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                   4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                   5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                   6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2201	99.9	401	3	US-09-062-113-5	Sequence 5, Appli
2	2201	99.9	401	4	US-10-183-091-1	Sequence 1, Appli
3	2201	99.9	401	4	US-10-364-045-1	Sequence 1, Appli
4	2201	99.9	401	4	US-10-232-858-5	Sequence 5, Appli
5	2201	99.9	401	4	US-10-377-076-1	Sequence 1, Appli
6	2201	99.9	401	4	US-10-785-109-5	Sequence 5, Appli
7	2201	99.9	401	4	US-10-785-114-5	Sequence 5, Appli
8	2201	99.9	401	5	US-10-929-958-5	Sequence 5, Appli
9	2201	99.9	401	5	US-10-929-748-5	Sequence 5, Appli
10	2201	99.9	401	5	US-10-979-303-5	Sequence 5, Appli
11	2201	99.9	401	5	US-10-979-654-5	Sequence 5, Appli
12	2201	99.9	401	6	US-11-231-963-1	Sequence 1, Appli
13	2201	99.9	401	6	US-11-254-836-1	Sequence 1, Appli
14	2195	99.7	401	4	US-10-066-209-1	Sequence 1, Appli
15	2195	99.7	401	4	US-10-105-934-2	Sequence 2, Appli
16	2195	99.7	401	4	US-10-164-592-2	Sequence 2, Appli
17	2195	99.7	401	4	US-10-044-674-3	Sequence 3, Appli
18	2195	99.7	401	4	US-10-322-673-5	Sequence 5, Appli
19	2195	99.7	401	4	US-10-139-785-5	Sequence 5, Appli
20	2195	99.7	401	5	US-10-895-676-2	Sequence 2, Appli
21	2195	99.7	401	5	US-10-986-046-5	Sequence 5, Appli
22	2195	99.7	401	5	US-10-986-047-5	Sequence 5, Appli
23	2195	99.7	401	5	US-10-966-845-2	Sequence 2, Appli
24	2195	99.7	401	5	US-10-775-204-528	Sequence 528, App
25	2195	99.7	401	5	US-10-775-204-529	Sequence 529, App
26	2195	99.7	401	5	US-10-775-204-542	Sequence 542, App
27	2195	99.7	401	5	US-10-775-204-1238	Sequence 1238, Ap
28	2195	99.7	401	5	US-10-775-204-1239	Sequence 1239, Ap
29	2195	99.7	401	5	US-10-775-204-1240	Sequence 1240, Ap
30	2195	99.7	401	5	US-10-775-204-1241	Sequence 1241, Ap
31	2195	99.7	401	5	US-10-775-204-1242	Sequence 1242, Ap
32	2195	99.7	401	5	US-10-775-204-1243	Sequence 1243, Ap
33	2195	99.7	401	5	US-10-775-204-1244	Sequence 1244, Ap
34	2195	99.7	401	5	US-10-775-204-1245	Sequence 1245, Ap
35	2195	99.7	401	5	US-10-981-465-5	Sequence 5, Appli
36	2195	99.7	401	5	US-10-981-621-5	Sequence 5, Appli
37	2195	99.7	401	5	US-10-981-673-5	Sequence 5, Appli
38	2195	99.7	401	5	US-10-981-691-5	Sequence 5, Appli
39	2195	99.7	401	5	US-10-986-349-5	Sequence 5, Appli
40	2195	99.7	401	5	US-10-986-376-5	Sequence 5, Appli
41	2195	99.7	401	5	US-10-510-876-2	Sequence 2, Appli
42	2195	99.7	401	5	US-10-921-793-52	Sequence 52, Appl
43	2195	99.7	401	5	US-10-931-198-52	Sequence 52, Appl
44	2195	99.7	401	5	US-10-942-042-52	Sequence 52, Appl
45	2195	99.7	986	5	US-10-775-204-312	Sequence 312, App

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rapbn.

start

```
                          GenCore version 5.1.9
                 Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:          July 11, 2006, 06:44:06 ; Search time 15.1 Seconds
                                           (without alignments)
                                           642.903 Million cell updates/sec

Title:           US-10-785-114-6
Perfect score:   2202
Sequence:        1 atgaacaacttgctgtgctg..........taaaaataagctgcttataa 1206

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters:       225884

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10785114/runat_11072006_062832_21607/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05p
-USER=US10785114_@CGN_1_1_12_@runat_11072006_062832_21607 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Published_Applications_AA_New:*
                 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

          Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2195	99.7	401	7	US-11-175-714-54	Sequence 54, Appl
2	1726.5	78.4	349	7	US-11-175-714-67	Sequence 67, Appl
3	347	15.8	258	6	US-10-643-589-4	Sequence 4, Appli
4	340	15.4	355	6	US-10-504-973-33	Sequence 33, Appl
5	330	15.0	461	6	US-10-511-937-2945	Sequence 2945, Ap
6	330	15.0	461	7	US-11-183-218-32	Sequence 32, Appl
7	301.5	13.7	655	6	US-10-505-928-843	Sequence 843, App
8	301.5	13.7	655	6	US-10-196-749-418	Sequence 418, App
9	287.5	13.1	289	7	US-11-170-797-12	Sequence 12, Appl
10	267	12.1	278	7	US-11-170-797-16	Sequence 16, Appl
11	264	12.0	197	7	US-11-211-917-139	Sequence 139, App
12	264	12.0	277	6	US-10-511-937-2518	Sequence 2518, Ap
13	264	12.0	277	7	US-11-170-797-5	Sequence 5, Appli
14	257.5	11.7	237	6	US-10-504-973-22	Sequence 22, Appl
15	252.5	11.5	269	7	US-11-170-797-19	Sequence 19, Appl
16	198	9.0	153	7	US-11-211-917-140	Sequence 140, App
17	188.5	8.6	250	7	US-11-320-192-7	Sequence 7, Appli
18	188	8.5	256	6	US-10-623-808-6	Sequence 6, Appli
19	188	8.5	256	7	US-11-128-422-6	Sequence 6, Appli
20	187.5	8.5	243	7	US-11-320-192-9	Sequence 9, Appli
21	187.5	8.5	243	7	US-11-320-192-12	Sequence 12, Appl
22	187.5	8.5	251	7	US-11-320-192-8	Sequence 8, Appli
23	186.5	8.5	250	7	US-11-320-192-11	Sequence 11, Appl
24	184.5	8.4	250	7	US-11-320-192-10	Sequence 10, Appl
25	177	8.0	255	6	US-10-623-808-8	Sequence 8, Appli
26	177	8.0	255	6	US-10-539-257-2	Sequence 2, Appli
27	177	8.0	255	7	US-11-128-422-8	Sequence 8, Appli
28	174	7.9	277	6	US-10-511-937-2455	Sequence 2455, Ap
29	168	7.6	247	6	US-10-504-973-6	Sequence 6, Appli
30	154	7.0	440	7	US-11-254-182-49	Sequence 49, Appl
31	144.5	6.6	468	6	US-10-511-937-2595	Sequence 2595, Ap
32	143	6.5	241	7	US-11-351-617-4	Sequence 4, Appli
33	143	6.5	241	7	US-11-315-825-3	Sequence 3, Appli
34	142.5	6.5	411	7	US-11-254-182-47	Sequence 47, Appl
35	142.5	6.5	411	7	US-11-297-319-1	Sequence 1, Appli
36	138	6.3	228	7	US-11-351-617-6	Sequence 6, Appli
37	138	6.3	311	7	US-11-351-617-8	Sequence 8, Appli
38	125	5.7	417	6	US-10-505-928-793	Sequence 793, App
39	123	5.6	228	7	US-11-351-617-2	Sequence 2, Appli
40	123	5.6	228	7	US-11-315-825-24	Sequence 24, Appl
41	121.5	5.5	969	6	US-10-505-928-94	Sequence 94, Appl
42	119	5.4	111	7	US-11-211-917-141	Sequence 141, App
43	116	5.3	1418	7	US-11-217-997-38	Sequence 38, Appl
44	114.5	5.2	408	7	US-11-175-714-140	Sequence 140, App
45	114.5	5.2	430	7	US-11-175-714-138	Sequence 138, App

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rpr.
start

```
                            GenCore version 5.1.9
                  Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:          July 11, 2006, 06:38:44 ; Search time 5.8 Seconds
                                            (without alignments)
                                            6001.935 Million cell updates/sec

Title:           US-10-785-114-6
Perfect score:   2202
Sequence:        1 atgaacaacttgctgtgctg..........taaaaataagctgcttataa 1206

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries.

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10785114/runat_11072006_062823_21423/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10785114_@CGN_1_1_32_@runat_11072006_062823_21423 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                            SUMMARIES
      %
```

Result No.	Score	Query Match	Length	DB	ID	Description
1	344	15.6	474	2	B38634	tumor necrosis fac
2	343	15.6	459	2	I48854	gene murine tumour
3	330	15.0	461	1	A35356	tumor necrosis fac
4	329	14.9	651	2	JC7705	death receptor-6 -
5	287.5	13.1	305	2	A46476	B cell-associated
6	264	12.0	277	2	A60771	B-cell activation
7	239.5	10.9	435	2	I54182	tumor necrosis fac
8	237	10.8	348	2	T28623	hypothetical prote
9	231.5	10.5	349	2	D36858	gene G4R protein -
10	228.5	10.4	349	2	D72175	G2R protein - vari
11	225	10.2	325	2	B43692	T2 protein - rabbi
12	219	9.9	326	1	GQVZML	T2 protein - myxom
13	189.5	8.6	425	1	A26431	nerve growth facto
14	188.5	8.6	427	1	GQHUN	nerve growth facto
15	188	8.5	256	2	B32393	T-cell antigen 4-1
16	187	8.5	461	1	GQRTT1	tumor necrosis fac
17	185.5	8.4	314	2	I37383	FAS soluble protei
18	183	8.3	335	2	A40036	apoptosis-mediatin
19	177.5	8.1	416	1	JN0006	nerve growth facto
20	177	8.0	255	2	I38426	lymphocyte activat
21	176	8.0	454	1	GQMST1	tumor necrosis fac
22	174	7.9	277	2	I37552	OX40 homolog - hum
23	173.5	7.9	455	1	GQHUT1	tumor necrosis fac
24	172	7.8	271	2	S12783	OX40 antigen precu
25	168	7.6	461	2	JC4302	tumor necrosis fac
26	158	7.2	595	2	A42086	CD30 antigen precu
27	152.5	6.9	272	2	I48700	gene ox40 protein
28	152	6.9	324	2	JC2395	Fas antigen precur
29	145	6.6	643	2	T25473	hypothetical prote
30	144	6.5	327	2	A46484	apoptosis-mediatin
31	142.5	6.5	1548	2	S34583	serine proteinase'
32	137.5	6.2	2823	2	F87908	protein T22A3.8 [i
33	137.5	6.2	2823	2	T23064	hypothetical prote
34	137.5	6.2	3102	2	T43291	laminin alpha chai
35	133	6.0	1252	2	S36016	oocyst wall protei
36	130	5.9	398	2	T33383	hypothetical prote
37	129.5	5.9	1369	2	S70713	protein-tyrosine k
38	129.5	5.9	1786	1	MMHUB1	laminin beta-1 cha
39	129.5	5.9	2610	2	T20968	hypothetical prote
40	129.5	5.9	2918	2	A54105	fibrillin-2 precur
41	129	5.9	1790	1	MMFFB1	laminin beta-1 cha
42	128.5	5.8	899	2	G02428	subtilisin-like pr
43	128.5	5.8	915	2	JC6148	subtilisin-like pr
44	128	5.8	3712	2	S18253	laminin alpha-1 ch
45	125.5	5.7	1786	1	MMMSB1	laminin beta-1 cha

This page gives you Search Results detail for the Application 10785114 and Search Result us-10-785-114-6.rup.

start

```
                      GenCore version 5.1.9
            Copyright (c) 1993 - 2006  Biocceleration Ltd.


OM nucleic - protein search, using frame_plus_n2p model

Run on:          July 11, 2006, 06:35:56 ; Search time 44.9 Seconds
                                            (without alignments)
                                 7453.689 Million cell updates/sec

Title:           US-10-785-114-6
Perfect score:   2202
Sequence:        1 atgaacaacttgctgtgctg..........taaaaataagctgcttataa 1206

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:     5699196

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10785114/runat_11072006_062820_21400/app_query.fasta_1
-DB=UniProt -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10785114_@CGN_1_1_381_@runat_11072006_062820_21400 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       UniProt_7.2:*
                 1:  uniprot_sprot:*
                 2:  uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES
                        %
Result          Query
  No.   Score  Match Length DB  ID                        Description
```

1	2201	99.9	401	2	Q53FX6_HUMAN	Q53fx6	homo sapien
2	2195	99.7	401	1	TR11B_HUMAN	O00300	homo sapien
3	1909	86.7	401	1	TR11B_RAT	O08727	rattus norv
4	1909	86.7	401	2	Q6PI12_MOUSE	Q6pi12	mus musculu
5	1895	86.1	401	1	TR11B_MOUSE	O08712	mus musculu
6	1895	86.1	401	2	Q3UK97_MOUSE	Q3uk97	m 11 days p
7	1596.5	72.5	402	2	Q4F9K2_CHICK	Q4f9k2	gallus gall
8	1038.5	47.2	387	2	Q6GLN3_XENLA	Q6gln3	xenopus lae
9	608	27.6	146	2	Q7ZZY4_CHICK	Q7zzy4	gallus gall
10	584.5	26.5	480	2	Q4SH87_TETNG	Q4sh87	tetraodon n
11	450	20.4	186	2	Q7ZZY5_CHICK	Q7zzy5	gallus gall
12	445	20.2	300	1	TNR6B_HUMAN	O95407	homo sapien
13	408.5	18.6	302	2	Q9PUS0_SALFO	Q9pus0	salvelinus
14	380.5	17.3	285	2	Q90W71_ONCMY	Q90w71	oncorhynchu
15	372.5	16.9	285	2	Q90YS6_ONCMY	Q90ys6	oncorhynchu
16	364	16.5	286	2	Q6NW61_BRARE	Q6nw61	brachydanio
17	354	16.1	561	2	Q4SH86_TETNG	Q4sh86	tetraodon n
18	347	15.8	474	2	Q3U2A9_MOUSE	Q3u2a9	mus musculu
19	344	15.6	474	1	TNR1B_MOUSE	P25119	mus musculu
20	344	15.6	474	2	Q545P4_MOUSE	Q545p4	m adult mal
21	344	15.6	637	2	Q5TYN2_BRARE	Q5tyn2	brachydanio
22	343	15.6	459	2	Q62327_MOUSE	Q62327	mus musculu
23	333	15.1	461	2	Q6VAU8_RAT	Q6vau8	rattus norv
24	333	15.1	474	1	TNR1B_RAT	Q80wy6	rattus norv
25	333	15.1	474	2	Q5YLP0_RAT	Q5ylp0	rattus norv
26	330	15.0	461	1	TNR1B_HUMAN	P20333	h tumor nec
27	330	15.0	461	2	Q5THJ6_HUMAN	Q5thj6	homo sapien
28	329	14.9	651	2	Q98SM6_CHICK	Q98sm6	gallus gall
29	322.5	14.6	433	2	Q91ZM6_RAT	Q91zm6	rattus norv
30	301.5	13.7	655	1	TNR21_HUMAN	O75509	homo sapien
31	298	13.5	483	2	Q800K7_PAROL	Q800k7	paralichthy
32	297	13.5	457	2	Q8IVS6_HUMAN	Q8ivs6	homo sapien
33	295	13.4	655	2	Q3UYG3_MOUSE	Q3uyg3	mus musculu
34	294	13.4	267	2	Q3UPV2_MOUSE	Q3upv2	mus musculu
35	294	13.4	459	2	Q3MHI9_BOVIN	Q3mhi9	bos taurus
36	294	13.4	655	1	TNR21_MOUSE	Q9epu5	mus musculu
37	294	13.4	655	2	Q543Y9_MOUSE	Q543y9	mus musculu
38	293	13.3	289	2	Q3U7C9_MOUSE	Q3u7c9	mus musculu
39	292.5	13.3	289	2	Q4QQW2_RAT	Q4qqw2	rattus norv
40	291.5	13.2	289	2	Q3U799_MOUSE	Q3u799	mus musculu
41	290.5	13.2	289	2	Q3TSL2_MOUSE	Q3tsl2	m 10 days n
42	290.5	13.2	289	2	Q3UBH3_MOUSE	Q3ubh3	mus musculu
43	290.5	13.2	289	2	Q8K2X6_MOUSE	Q8k2x6	mus musculu
44	287.5	13.1	289	1	TNR5_MOUSE	P27512	mus musculu
45	287.5	13.1	289	2	Q542B1_MOUSE	Q542b1	m activated